Attorney's Docket No.: 09010-910001

OFFICIAL COMMUNICATION
FACSIMILE
FOR THE PERSONAL ATTENTION OF:
EXAMINER MICHAEL L. BORIN
U.S. PATENT AND TRADEMARK OFFICE (PATENT)
COMMISSIONER FOR PATENTS
P.O. BOX 1450
ALEXANDRIA, VA 22313-1450

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GROUP 1646 FAX NO: 703 872-9306

Number of pages including this page 5

Applicant : Short, et al.   Art Unit : 1646
Serial No. : 09/997,807   Examiner : Michael Borin, Ph.D.
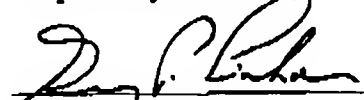Filed : November 30, 2001

FACSIMILE COMMUNICATION

Title : Method of Making a Protein Polymer and Uses of the Polymer

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

Attached to this facsimile communication cover sheet is an Appendix A to supplement Applicants' Preliminary Amendment and Response to Restriction Requirement faxed yesterday October 29, 2003; this Appendix A being faxed this 30th day of October, 2003, to Group 1646, the United States Patent and Trademark Office.

Respectfully submitted,

Gregory P. Einhorn
Reg. No. 38,440

Date:October 30, 2003

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CLUSTAL W (1.81) Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: SEQID_1   624 bp
Sequence 2: SEQID_3   513 bp
Sequence 3: SEQID_5   537 bp
Sequence 4: SEQID_7   395 bp
Sequence 5: SEQID_9   372 bp
Start of Pairwise alignments
Aligning...
Sequences (2:3) Aligned. Score: 78
Sequences (1:2) Aligned. Score: 80
Sequences (4:5) Aligned. Score: 70
Sequences (3:4) Aligned. Score: 67
Sequences (2:4) Aligned. Score: 66
Sequences (3:5) Aligned. Score: 78
Sequences (2:5) Aligned. Score: 79
Sequences (1:3) Aligned. Score: 76
Sequences (1:4) Aligned. Score: 62
Sequences (1:5) Aligned. Score: 63
Guide tree   file created: [clustalw.dnd]
Start of Multiple Alignment
There are 4 groups
Aligning...
Group 1: Sequences: 2   Score:5182
Group 2: Sequences: 2   Score:7433
Group 3: Sequences: 3   Score:7603
Group 4: Sequences: 5   Score:4901
Alignment Score 20690
CLUSTAL-Alignment file created [clustalw.aln]
CLUSTAL W (1.81) multiple sequence alignment

SEQID_7   --
SEQID_9   --
SEQID_1   GTGAAGTACACAACCCTAGCTATAGCGGGTATTATTGCCTCGGCTGCCGCCCTCGCCCTC
SEQID_3   GTGAAGCCTACGGCTCTAGCCCTGGCTGGTATCATTGCCTCGGCTGCCGACCTCGCCCTG
SEQID_5   ATGAGGTACACGACCCTAGCTCTGGCCGGCATAGTGGCCTCGGCTGCCGCCCTCGCCCTG

SEQID_7   --AGCTTCTACGCCACCGGCACAGCA
SEQID_9   --AGCTTCTACGCCACCGGCACAGCA
SEQID_1   CTAGCAGGCTTCGCCACCACCCAGAGCCCCCTCAACAGCTTCTACGCCACCGGTACAGCA
SEQID_3   CTAGCAGGCTTCGCCACCACCCAGAGCCCGCTCAACAGCTTCTACGCCACCGGCACAGCA
SEQID_5   CTAGCAGGCTTCGCCACGACCCAGAGCCCGCTAAGCAGCTTCTACGCCACCGGCACAGCA
                                                 ****************** ******

SEQID_7   CAGGCAGTAAGCGAGCCAATAGACGTGGTAAGCAGCCTCGGTACG---CTAAATACTGCC
SEQID_9   GAGGCAACAAGCGAGCCAATAGACGTTGTAAGCAACCTTAACACGGCCATAGCCCCTGCT
SEQID_1   CAGGCAGTAAGCGAGCCAATAGACGTAGAAAGCCACCT---CGGCAGCATAACCCCCGCA
SEQID_3   GCCGCAACAAGCGAGCCAATAGACGTAGAGAGCCACCT---CAGCAGCATAGCCCCTGCT
SEQID_5   CAAGCAGTAAGCGAGCCAATAGACGTAGAGAGCCACCTAGACAACACCATAGCCCCTGCT
                ***   ***************** *   *** ***   **   * **

```
SEQID_7   GCTGGTGCACAGGGTAAGCAGACGCTAGGAGACATAACAATATATGCGCACAATGACGTG
SEQID_9   GCCGGCGCCCAGGGCAGCGTGGGCATAGGCAGCATAACAATAGAGAACAAGACTGACGTG
SEQID_1   GCCGGCGCACAGGGCAGTGACGACATAGGTTACGCAATAGTGTGGATAAAGGACCAGGTC
SEQID_3   GCTGGCGCACAGGGCAGCCAGGACATAGGCTACTTCAACGTGACCGCCAAGGATCAAGTG
SEQID_5   GCCGGTGCACAGGGCTACAAGGACATGGGCTACATTAAGATAACTAACCAGTCAAAAGTT
          **  ** **  *****       *  **   *   *   *        *     *  **

SEQID_7   AACATAACAAAGCTAAAGGTCACGCTTGCTAACGCTGCACAGCTAAGACCATACTTCAAG
SEQID_9   AACGTTGTGAAGCTGAAGATAACCCTCGCCAACGCTGAGCAGCTAAAGCCCTACTTCGAC
SEQID_1   AATGATGTAAAGCTGAAGGTGACCCTGCGTAACGCTGAGCAGCTAAAGCCCTACTTCAAG
SEQID_3   AACGTGACAAAGATAAAGGTGACCCTGGCTAACGCTGAGCAGCTAAAGCCCTACTTCAAG
SEQID_5   AATGTAATAAAGCTGAAGGTGACTCTCGCTAACGCCGAGCAGCTAAAGCCCTACTTCGAC
          **           ***  *  *** *  ** **      ***** *  ******* **  ****** *

SEQID_7   TACCTGATAATAAAGCTAGTAAGCCTGGAC--------------AGCAACGGCAACGAG
SEQID_9   TACCTACAGATAGTGCTAAAGAGCGTTGAC--------------AGCAACGAGATCAAG
SEQID_1   TACCTACAGATACAGATAACAAGCGGCTATGAGACGAACAGCACAGCTCTAGGCAACTTC
SEQID_3   TACCTACAGATAGTGCTAAAGAGCG-----------------------AGGTAGCT--
SEQID_5   TACCTACAGCTAGTACTCACAAGCAAC----------------GCCACTGGCACC---
          *****      **    *    ***                         *  *  *

SEQID_7   TCCGAGGAAAAGGGCATGATAACTCTATGCAAGCCTTACGCCGTGATAATACTAGACCAT
SEQID_9   GCTG-----------TGCTAAGCCTCGAGAAGCCCAGCGCAGTCATAATACTGGACAAC
SEQID_1   AGCGAGACCAAGGCTGTGATAAGCCTCGACAACCCCAGCGCCGTGATAGTACTAGACAAG
SEQID_3   GACGAGATCAAGGCCGTAATAAGCATAGACAAGCCTAGCGCCGTCATAATACTAGACAGC
SEQID_5   GACATGGTTAAGGCTGTGCTAAGCCTCGAGAAGCCTAGCGCAGTCATAATACTAGACAAC
              *   ***   *     ** **   *** **  *** **** ***

SEQID_7   GAAGA---------------------------------------TTTCAACAACGACA
SEQID_9   GAGGA---------------------------------------CTTCCAG-------
SEQID_1   GAGGATATAGCAGTGCTCTATCCGGACAAGACCGGTTACACAAACACTTCGATATGGGTA
SEQID_3   CAGGA---------------------------------------CTTCGACAG-----
SEQID_5   GATGA---------------------------------------CTACGATAG-----
          *  **                                        *  *  *

SEQID_7   TC------------GACAATGACGGCAACAATGACGCCAAGATA------------AGG
SEQID_9   ---------------------GGCGGCGACAACCAGTGCCAGATA-----------GAC
SEQID_1   CCCGGTGAACCTGACAAGATAATTGTCTACAACGAGACAAAGCCAGTAGCTATACTGAAC
SEQID_3   --------------------------CAACAACAGAGCAAAGATA------------AGC
SEQID_5   --------------------CACTAACAAGATACAGCTA-----------AAG
                              *    **        **  *

SEQID_7   GTTGTAGCCTACTATGAGGCTAAGGAGGGTATGCT------------------------
SEQID_9   GCCACCGCCTACTACGAGGCTAAGGAGGGTATGCTA-----------------------
SEQID_1   TTCAAGGCCTTCTACGAGGCTAAGGAGGGTATGCTATTCGACAGCCTGCCAGTGATATTC
SEQID_3   GCCACTGCCTACTACGAGGCTAAGGAGGGCATGCTATTCGACAGCCTACCGCTAATATTC
SEQID_5   GTAGAAGCCTACTATGAGGCTAAGGAGGGCATGCTATTCGACAGCCTACCAGTAATACTG
          ****  *** **************** *****

SEQID_7   ------------------------------------------------
SEQID_9   ------------------------------------------------
SEQID_1   AACTTCCAGGTGCTACAAGTAGGCTAA---------------
SEQID_3   AACATACAGGTGCTAAGCGTCAGCTAA---------------
SEQID_5   AACTTCCAGGTACTGAGCGCCGCTTGCAGTCCCTTGTGGTGA
```

(
(

```
(
SEQID_1:0.13368,
SEQID_3:0.05931)
:0.04152,
SEQID_5:0.08657)
:0.03782,
SEQID_7:0.18976,
SEQID_9:0.10325);
```

CLUSTAL W (1.81) Multiple Sequence Alignments

```
Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: SEQID_2        207 aa
Sequence 2: SEQID_4        170 aa
Sequence 3: SEQID_6        178 aa
Sequence 4: SEQID_8        131 aa
Sequence 5: SEQID_10       124 aa
Start of Pairwise alignments
Aligning...
Sequences (4:5) Aligned. Score:  63
Sequences (2:3) Aligned. Score:  70
Sequences (3:4) Aligned. Score:  54
Sequences (2:4) Aligned. Score:  58
Sequences (3:5) Aligned. Score:  68
Sequences (2:5) Aligned. Score:  70
Sequences (1:2) Aligned. Score:  72
Sequences (1:3) Aligned. Score:  65
Sequences (1:4) Aligned. Score:  54
Sequences (1:5) Aligned. Score:  60
Guide tree        file created:    [clustalw.dnd]
Start of Multiple Alignment
There are 4 groups
Aligning...
Group 1: Sequences:    2       Score:2421
Group 2: Sequences:    3       Score:2348
Group 3: Sequences:    4       Score:1624
Group 4: Sequences:    5       Score:946
Alignment Score 4564
CLUSTAL-Alignment file created  [clustalw.aln]
CLUSTAL W (1.81) multiple sequence alignment


SEQID_1    VKYTTLAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLG-SITPA
SEQID_3    VKPTALALAGIIASAADLALLAGFATTQSPLNSFYATGTAAATSEPIDVESHLS-SIAPA
SEQID_5    MRYTTLALAGIVASAAALALLAGFATTQSPLSSFYATGTAQAVSEPIDVESHLDNTIAPA
SEQID_9    ------------------------------------SPYATGTAEATSEPIDVVSNLNTAIAPA
SEQID_7    ------------------------------------SPYATGTAQAVSEPIDVVSSLG-TLNTA
                                                   ******** *.****** * *. :: .*
```

```
SEQID_1    AGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALGNF
SEQID_3    AGAQGSQDIGYFNVTAKDQVNVTKIKVTLANAEQLKPYFKYLQIVLKS---------EVA
SEQID_5    AGAQGYKDMGYIKITNQSKVNVIKLKVTLANAAEQLKPYPDYLQLVLTSN-------ATGT
SEQID_9    AGAQGSVGIGSITIENKTDVNVVKLKITLANAEQLKPYFDYLQIVLKSVD--------S
SEQID_7    AGAQGKQTLGDITIYAHNDVNITKLKVTLANAAQLRPYFKYLIIKLVSLD-----SNGNE
           *****    :*     :   :  .**   *:*:**  **  **:***.**  :  :  *

SEQID_1    SETKAVISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIVYNETKPVAILN
SEQID_3    DEIKAVISIDKPSAVIILDSQDFDSNNRAKISAT--------------------------
SEQID_5    DMVKAVLSLEKPSAVIILDNDDYDSTNKIQLKVE--------------------------
SEQID_9    NEIKAVLSLEKPSAVIILDNEDFQGGDNQCQIDAT-------------------------
SEQID_7    SEEKGMITLWKPYAVIILDHEDFNNDIDNDGNNDAKIR----------------------
           .  *.::::  :*  ***:**  :*

SEQID_1    PKAFYEAKEGMLFDSLPVIFNFQVLQVG-----
SEQID_3    --AYYEAKEGMLFDSLPLIPNIQVLSVS-----
SEQID_5    --AYYEAKEGMLFDSLPVILNFQVLSAACSPLW
SEQID_9    --AYYEAKEGML---------------------
SEQID_7    VVAYYEAKEGM---------------------
           *;*******
```

```
(
(
SEQID_1:0.16476,
SEQID_3:0.10583)
:0.02956,
SEQID_5:0.15636,
(
SEQID_7:0.23354,
SEQID_9:0.12936)
:0.04464);
```